

ENTERED



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RAW SEQUENCE LISTING

DATE: 05/30/2002

PATENT APPLICATION: US/09/974,973

TIME: 09:24:49

Input Set : A:\seqlist_1533 1230001.txt

Output Set : N:\CRF3\05302002\I974973.raw

5 <110> APPLICANT: Hanke, Paul D.
9 <120> TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from
Corynebacterium
13 <130> FILE REFERENCE: 1533.1230001/MAC/RGM
17 <140> CURRENT APPLICATION NUMBER: US 09/974,973
C--> 19 <141> CURRENT FILING DATE: 2001-10-21
23 <150> PRIOR APPLICATION NUMBER: US 60/239,913
25 <151> PRIOR FILING DATE: 2000-10-13
29 <160> NUMBER OF SEQ ID NOS: 19
33 <170> SOFTWARE: PatentIn version 3.0
37 <210> SEQ ID NO: 1
39 <211> LENGTH: 3474
41 <212> TYPE: DNA
43 <213> ORGANISM: Corynebacterium glutamicum
47 <220> FEATURE:
49 <221> NAME/KEY: CDS
51 <222> LOCATION: (1)..(3474)
55 <400> SEQUENCE: 1

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57	Met Thr Ala Ile Thr Leu Gly Gly Leu Leu Lys Gly Ile Ile Thr	
58	1 5 10 15	
60	cta gtg tcg act cac aca tct tca acg ctt cca gca ttc aaa aag atc	96
61	Leu Val Ser Thr His Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile	
62	20 25 30	
63	ttg gta gca aac cgc ggc gaa atc gcg gtc cgt gct ttc cgt gca gca	144
64	Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala	
65	35 40 45	
67	ctc gaa acc ggt gca gcc acg gta gct att tac ccc cgt gaa gat cgg	192
68	Leu Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg	
69	50 55 60	
71	gga tca ttc cac cgc tct ttt gct tct gaa gct gtc cgc att ggt act	240
72	Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr	
73	65 70 75 80	
75	gaa ggc tca cca gtc aag gcg tac ctg gac atc gat gaa att atc ggt	288
76	Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly	
77	85 90 95	
79	gca gct aaa aaa gtt aaa gca gat gct att tac ccg gga tat ggc ttc	336
80	Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe	
81	100 105 110	
83	ctg tct gaa aat gcc cag ctt gcc cgc gag tgc gcg gaa aac ggc att	384
84	Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile	
85	115 120 125	
87	act ttt att ggc cca acc cca gag gtt ctt gat ctc acc ggt gat aag	432
88	Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys	

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89	130	135	140	
91	tct cgt gcg gta acc gcc gcg aag aag gct ggt ctg cca gtt ttg gcg	480		
92	Ser Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala			
93	145	150	155	160
95	gaa tcc acc ccg agc aaa aac atc gat gac atc gtt aaa agc gct gaa	528		
96	Glu Ser Thr Pro Ser Lys Asn Ile Asp Asp Ile Val Lys Ser Ala Glu			
97	165	170	175	
99	ggc cag act tac ccc atc ttt gta aag gca gtt gcc ggt ggt ggc gga	576		
100	Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly			
101	180	185	190	
103	cgc ggt atg cgc ttt gtt tct tca cct gat gag ctc cgc aaa ttg gca	624		
104	Arg Gly Met Arg Phe Val Ser Ser Pro Asp Glu Leu Arg Lys Leu Ala			
105	195	200	205	
107	aca gaa gca tct cgt gaa gct gaa gcg gca ttc ggc gac ggt tgc gta	672		
108	Thr Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ser Val			
109	210	215	220	
111	tat gtc gaa cgt gct gtg att aac ccc cag cac att gaa gtg cag atc	720		
112	Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile			
113	225	230	235	240
115	ctt ggc gat cgc act gga gaa gtt gta cac ctt tat gaa cgt gac tgc	768		
116	Leu Gly Asp Arg Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys			
117	245	250	255	
119	tca ctg cag cgt cgt cac caa aaa gtt gtc gaa att gcg cca gca cag	816		
120	Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln			
121	260	265	270	
123	cat ttg gat cca gaa ctg cgt gat cgc att tgt gcg gat gca gta aag	864		
124	His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys			
125	275	280	285	
127	ttc tgc cgc tcc att ggt tac cag ggc gcg gga acc gtg gaa ttc ttg	912		
128	Phe Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu			
129	290	295	300	
131	gtc gat gaa aag ggc aac cac gtt ttc atc gaa atg aac cca cgt atc	960		
132	Val Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile			
133	305	310	315	320
135	cag gtt gag cac acc gtg act gaa gaa gtc acc gag gtg gac ctg gtg	1008		
136	Gln Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val			
137	325	330	335	
139	aag gcg cag atg cgc ttg gct gct ggt gca acc ttg aag gaa ttg ggt	1056		
140	Lys Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly			
141	340	345	350	
143	ctg acc caa gat aag atc aag acc cac ggt gca gca ctg cag tgc cgc	1104		
144	Leu Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg			
145	355	360	365	
147	atc acc acg gaa gat cca aac aac ggc ttc cgc cca gat acc gga act	1152		
148	Ile Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr			
149	370	375	380	
151	atc acc gcg tac cgc tca cca ggc gga gct ggc gtt cgt ctt gac ggt	1200		
152	Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly			
153	385	390	395	400

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155	gca	gct	cag	ctc	ggt	ggc	gaa	atc	acc	gca	cac	ttt	gac	tcc	atg	ctg	1248
156	Ala	Ala	Gln	Leu	Gly	Gly	Glu	Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu	
157				405						410				415			
159	gtg	aaa	atg	acc	tgc	cgt	ggt	tcc	gac	ttt	gaa	act	gct	gtt	gct	cgt	1296
160	Val	Lys	Met	Thr	Cys	Arg	Gly	Ser	Asp	Phe	Glu	Thr	Ala	Val	Ala	Arg	
161				420					425					430			
163	gca	cag	cgc	gcg	ttg	gct	gag	ttc	acc	gtg	tct	ggt	gtt	gca	acc	aac	1344
164	Ala	Gln	Arg	Ala	Leu	Ala	Glu	Phe	Thr	Val	Ser	Gly	Val	Ala	Thr	Asn	
165				435				440						445			
167	att	ggt	ttc	ttg	cgt	gcg	ttg	ctg	cgg	gaa	gag	gac	ttc	act	tcc	aag	1392
168	Ile	Gly	Phe	Leu	Arg	Ala	Leu	Leu	Arg	Glu	Glu	Asp	Phe	Thr	Ser	Lys	
169		450					455						460				
171	cgc	atc	gcc	acc	gga	ttt	atc	ggc	gat	cac	cca	cac	ctc	ctt	cag	gct	1440
172	Arg	Ile	Ala	Thr	Gly	Phe	Ile	Gly	Asp	His	Pro	His	Leu	Leu	Gln	Ala	
173	465				470					475					480		
175	cca	cct	gcg	gat	gat	gag	cag	gga	cgc	atc	ctg	gat	tac	ttg	gca	gat	1488
176	Pro	Pro	Ala	Asp	Asp	Glu	Gln	Gly	Arg	Ile	Leu	Asp	Tyr	Leu	Ala	Asp	
177				485					490					495			
179	gtc	acc	gtg	aac	aag	cct	cat	ggt	gtg	cgt	cca	aag	gat	gtt	gca	gca	1536
180	Val	Thr	Val	Asn	Lys	Pro	His	Gly	Val	Arg	Pro	Lys	Asp	Val	Ala	Ala	
181				500					505					510			
183	cca	atc	gat	aag	ctg	ccc	aac	atc	aag	gat	ctg	cca	ctg	cca	cgc	ggt	1584
184	Pro	Ile	Asp	Lys	Leu	Pro	Asn	Ile	Lys	Asp	Leu	Pro	Leu	Pro	Arg	Gly	
185			515				520						525				
187	tcc	cgt	gac	cgc	ctg	aag	cag	ctt	ggc	cca	gcc	gcg	ttt	gct	cgt	gat	1632
188	Ser	Arg	Asp	Arg	Leu	Lys	Gln	Leu	Gly	Pro	Ala	Ala	Phe	Ala	Arg	Asp	
189		530					535						540				
191	ctc	cgt	gag	cag	gac	gca	ctg	gca	gtt	act	gat	acc	ttc	cgc	gat		1680
192	Leu	Arg	Glu	Gln	Asp	Ala	Leu	Ala	Val	Thr	Asp	Thr	Thr	Phe	Arg	Asp	
193	545				550					555					560		
195	gca	cac	cag	tct	ttg	ctt	gcg	acc	cga	gtc	cgc	tca	ttc	gca	ctg	aag	1728
196	Ala	His	Gln	Ser	Leu	Leu	Ala	Thr	Arg	Val	Arg	Ser	Phe	Ala	Leu	Lys	
197				565					570					575			
199	cct	gcg	gca	gag	gcc	gtc	gca	aag	ctg	act	cct	gag	ctt	ttg	tcc	gtg	1776
200	Pro	Ala	Ala	Glu	Ala	Val	Ala	Lys	Leu	Thr	Pro	Glu	Leu	Leu	Ser	Val	
201				580					585					590			
203	gag	gcc	tgg	ggc	ggc	gcg	acc	tac	gat	gtg	gcg	atg	cgt	ttc	ctc	ttt	1824
204	Glu	Ala	Trp	Gly	Gly	Ala	Thr	Tyr	Asp	Val	Ala	Met	Arg	Phe	Leu	Phe	
205			595				600						605				
207	gag	gat	ccg	tgg	gac	agg	ctc	gac	gag	ctg	cgc	gag	gcg	atg	ccg	aat	1872
208	Glu	Asp	Pro	Trp	Asp	Arg	Leu	Asp	Glu	Leu	Arg	Glu	Ala	Met	Pro	Asn	
209		610					615						620				
211	gta	aac	att	cag	atg	ctg	ctt	cgc	ggc	cgc	aac	acc	gtg	gga	tac	acc	1920
212	Val	Asn	Ile	Gln	Met	Leu	Leu	Arg	Gly	Arg	Asn	Thr	Val	Gly	Tyr	Thr	
213	625				630					635					640		
215	ccg	tac	cca	gac	tcc	gtc	tgc	cgc	gcg	ttt	gtt	aag	gaa	gct	gcc	agc	1968
216	Pro	Tyr	Pro	Asp	Ser	Val	Cys	Arg	Ala	Phe	Val	Lys	Glu	Ala	Ala	Ser	
217				645					650					655			
219	tcc	ggc	gtg	gac	atc	ttc	cgc	atc	ttc	gac	gcg	ctt	aac	gac	gtc	tcc	2016

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220	Ser	Gly	Val	Asp	Ile	Phe	Arg	Ile	Phe	Asp	Ala	Leu	Asn	Asp	Val	Ser	
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223	cag	atg	cgt	cca	gca	atc	gac	gca	gtc	ctg	gag	acc	aac	acc	gcg	gta	2064
224	Gln	Met	Arg	Pro	Ala	Ile	Asp	Ala	Val	Leu	Glu	Thr	Asn	Thr	Ala	Val	
225			675					680					685				
227	gcc	gag	gtg	gct	atg	gct	tat	tct	ggg	gat	ctc	tct	gat	cca	aat	gaa	2112
228	Ala	Glu	Val	Ala	Met	Ala	Tyr	Ser	Gly	Asp	Leu	Ser	Asp	Pro	Asn	Glu	
229		690					695				700						
231	aag	ctc	tac	acc	ctg	gat	tac	tac	cta	aag	atg	gca	gag	gag	atc	gtc	2160
232	Lys	Leu	Tyr	Thr	Leu	Asp	Tyr	Tyr	Leu	Lys	Met	Ala	Glu	Glu	Ile	Val	
233	705				710					715					720		
235	aag	tct	ggc	gct	cac	att	ctg	gcc	att	aag	gat	atg	gct	ggg	ctg	ctt	2208
236	Lys	Ser	Gly	Ala	His	Ile	Leu	Ala	Ile	Lys	Asp	Met	Ala	Gly	Leu	Leu	
237				725					730				735				
239	cgc	cca	gct	gcg	gta	acc	aag	ctg	gtc	acc	gca	ctg	cgc	cgt	gaa	ttc	2256
240	Arg	Pro	Ala	Ala	Val	Thr	Lys	Leu	Val	Thr	Ala	Leu	Arg	Arg	Glu	Phè	
241				740					745				750				
243	gat	ctg	cca	gtg	cac	gtg	cac	acc	cac	gac	act	gcg	ggg	ggc	cag	ttg	2304
244	Asp	Leu	Pro	Val	His	Val	His	Thr	His	Asp	Thr	Ala	Gly	Gly	Gln	Leu	
245				755				760					765				
247	gct	acc	tac	ttt	gct	gca	gct	caa	gct	ggg	gca	gat	gct	gtt	gac	ggg	2352
248	Ala	Thr	Tyr	Phe	Ala	Ala	Ala	Gln	Ala	Gly	Ala	Asp	Ala	Val	Asp	Gly	
249		770				775				780							
251	gct	tcc	gca	cca	ctg	tct	ggc	acc	acc	tcc	cag	cca	tcc	ctg	tct	gcc	2400
252	Ala	Ser	Ala	Pro	Leu	Ser	Gly	Thr	Thr	Ser	Gln	Pro	Ser	Leu	Ser	Ala	
253	785				790					795					800		
255	att	gtt	gct	gca	ttc	gcg	cac	acc	cgt	cgc	gat	acc	ggg	ttg	agc	ctc	2448
256	Ile	Val	Ala	Ala	Phe	Ala	His	Thr	Arg	Arg	Asp	Thr	Gly	Leu	Ser	Leu	
257				805					810					815			
259	gag	gct	gtt	tct	gac	ctc	gag	ccg	tac	tgg	gaa	gct	gtg	cgc	gga	ctg	2496
260	Glu	Ala	Val	Ser	Asp	Leu	Glu	Pro	Tyr	Trp	Glu	Ala	Val	Arg	Gly	Leu	
261				820				825					830				
263	tac	ctg	cca	ttt	gag	tct	gga	acc	cca	ggc	cca	acc	ggg	cgc	gtc	tac	2544
264	Tyr	Leu	Pro	Phe	Glu	Ser	Gly	Thr	Pro	Gly	Pro	Thr	Gly	Arg	Val	Tyr	
265			835				840					845					
267	cgc	cac	gaa	atc	cca	ggc	gga	cag	ttg	tcc	aac	ctg	cgt	gca	cag	gcc	2592
268	Arg	His	Glu	Ile	Pro	Gly	Gly	Gln	Leu	Ser	Asn	Leu	Arg	Ala	Gln	Ala	
269		850				855					860						
271	acc	gca	ctg	ggc	ctt	gct	gat	cgc	ttc	gag	ctc	atc	gaa	gac	aac	tac	2640
272	Thr	Ala	Leu	Gly	Leu	Ala	Asp	Arg	Phe	Glu	Leu	Ile	Glu	Asp	Asn	Tyr	
273	865				870				875						880		
275	gca	gcc	gtt	aat	gag	atg	ctg	gga	cgc	cca	acc	aag	gtc	acc	cca	tcc	2688
276	Ala	Ala	Val	Asn	Glu	Met	Leu	Gly	Arg	Pro	Thr	Lys	Val	Thr	Pro	Ser	
277				885				890					895				
279	tcc	aag	gtt	gtt	ggc	gac	ctc	gca	ctc	cac	ctg	gtt	ggg	gcg	ggg	gta	2736
280	Ser	Lys	Val	Val	Gly	Asp	Leu	Ala	Leu	His	Leu	Val	Gly	Ala	Gly	Val	
281			900					905					910				
283	gat	cca	gca	gac	ttt	gct	gca	gac	cca	caa	aag	tac	gac	atc	cca	gac	2784
284	Asp	Pro	Ala	Asp	Phe	Ala	Ala	Asp	Pro	Gln	Lys	Tyr	Asp	Ile	Pro	Asp	

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287 tct gtc atc gcg ttc ctg cgc ggc gag ctt ggt aac cct cca ggt ggc      2832
288 Ser Val Ile Ala Phe Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly
289          930          935          940
291 tgg cca gaa cca ctg cgc acc cgc gca ctg gaa ggc cgc tcc gaa ggc      2880
292 Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly
293 945          950          955          960
295 aag gca cct ctg acg gaa gtt cct gag gaa gag cag gcg cac ctc gac      2928
296 Lys Ala Pro Leu Thr Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp
297          965          970          975
299 gct gat gat tcc aag gaa cgt cgc aac agc ctc aac cgc ctg ctg ttc      2976
300 Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe
301          980          985          990
303 ccg aag cca acc gaa gag ttc ctc gag cac cgt cgc cgc ttc ggc aac      3024
304 Pro Lys Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn
305          995          1000          1005
307 acc tct gcg ctg gat gat cgt gaa ttc ttc tac gga ctg gtc gag      3069
308 Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu
309          1010          1015          1020
311 ggc cgc gag act ttg atc cgc ctg cca gat gtg cgc acc cca ctg      3114
312 Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val Arg Thr Pro Leu
313          1025          1030          1035
315 ctt gtt cgc ctg gat gcg atc tct gag cca gac gat aag ggt atg      3159
316 Leu Val Arg Leu Asp Ala Ile Ser Glu Pro Asp Asp Lys Gly Met
317          1040          1045          1050
319 cgc aat gtt gtg gcc aac gtc aac ggc cag atc cgc cca atg cgt      3204
320 Arg Asn Val Val Ala Asn Val Asn Gly Gln Ile Arg Pro Met Arg
321          1055          1060          1065
323 gtg cgt gac cgc tcc gtt gag tct gtc acc gca acc gca gaa aag      3249
324 Val Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu Lys
325          1070          1075          1080
327 gca gat tcc tcc aac aag ggc cat gtt gct gca cca ttc gct ggt      3294
328 Ala Asp Ser Ser Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly
329          1085          1090          1095
331 gtt gtc act gtg act gtt gct gaa ggt gat gag gtc aag gct gga      3339
332 Val Val Thr Val Thr Val Ala Glu Gly Asp Glu Val Lys Ala Gly
333          1100          1105          1110
335 gat gca gtc gca atc atc gag gct atg aag atg gaa gca aca atc      3384
336 Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile
337          1115          1120          1125
339 act gct tct gtt gac ggc aag att gaa cgc gtt gtg gtt cct gct      3429
340 Thr Ala Ser Val Asp Gly Lys Ile Glu Arg Val Val Val Pro Ala
341          1130          1135          1140
343 gca acg aag gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taa      3474
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345          1145          1150          1155
348 <210> SEQ ID NO: 2
350 <211> LENGTH: 1157
352 <212> TYPE: PRT

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L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date